

Patent Application US/07/752,427

#2

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Grotendorst, Gary R.
Bradham Jr., Douglas M.,

(ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Spensley Horn Jubas & Lubitz

(B) STREET: 4225 Executive Square, Suite 1400

(C) CITY: La Jolla

(D) STATE: CA

(E) COUNTRY: US

(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US

(B) FILING DATE: 30-AUG-1991

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr: Ph.D., John W.

(B) REGISTRATION NUMBER: 31,678

(C) REFERENCE/DOCKET NUMBER: PD-1294

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-455-5100

(B) TELEFAX: 619-455-5110

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2075 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

OK

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54 (B) CLONE: DB60R32
55
56 (ix) FEATURE:
57 (A) NAME/KEY: CDS
58 (B) LOCATION: 130..1177
59
60
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
62
63 CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG 60
64
65 CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA 120
66
67 GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC 168
68 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe
69 1 5 10
70
71 GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC 216
72 Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys
73 15 20 25
74
75 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG 264
76 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala
77 30 35 40 45
78
79 GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC 312
80 Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala
81 50 55 60
82
83 AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC 360
84 Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His
85 65 70 75
86
87 AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC 408
88 Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly
89 80 85 90
90
91 GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG 456
92 Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val
93 95 100 105
94
95 TAC CGC AGC GGA GAG TCC TTC CAG AGC AGC TGC AAG TAC CAG TGC ACG 504
96 Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr
97 110 115 120 125
98
99 TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT 552
100 Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val
101 130 135 140
102
103 CGT CTG CCC AGC CCT GAC TGC CCC TTC CCG AGG AGG GTC AAG CTG CCC 600
104 Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro
105 145 150 155
106

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107	GGG AAA TGC TGC GAG GAG TGG GTG TGT GAC GAG CCC AAG GAC CAA ACC	648
108	Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr	
109	160 165 170	
110		
111	GTG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC	696
112	Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly	
113	175 180 185	
114		
115	CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG	744
116	Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu	
117	190 195 200 205	
118		
119	TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT	792
120	Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val	
121	210 215 220	
122		
123	ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG AGC CGC CTG TGC	840
124	Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys	
125	225 230 235	
126		
127	ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC	888
128	Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly	
129	240 245 250	
130		
131	AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG	936
132	Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu	
133	255 260 265	
134		
135	CTT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA	984
136	Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly	
137	270 275 280 285	
138		
139	GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG	1032
140	Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu	
141	290 295 300	
142		
143	CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG	1080
144	Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met	
145	305 310 315	
146		
147	ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT	1128
148	Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn	
149	320 325 330	
150		
151	GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T	1177
152	Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala	
153	335 340 345	
154		
155	GAAGCCAGAG AGTGAGAGAC ATTAATCAT TAGACTGGAA CTTGAACTGA TTCACATCTC	1237
156		
157	ATTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG	1297
158		
159	GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC	1357

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160
161 CCAGACACTG GTTGAAGAA TGTTAAGACT TGACAGTGGG ACTACATTAG TACACAGCAC 1417
162
163 CAGAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT 1477
164
165 CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA 1537
166
167 AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC 1597
168
169 CAGCCATCAA GAGACTGAGT CAAGTTGTTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA 1657
170
171 CATTCTGATT CGAATGACAC TGTTTCAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT 1717
172
173 TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTTA AAATTTATAT TGTAATATT 1777
174
175 GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA 1837
176
177 AGTTGTTTGT GCCTTTTAT TTTTGTTTTT AATGCTTTGA TATTTCAATG TTAGCCTCAA 1897
178
179 TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT 1957
180
181 ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAA 2017
182
183 GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG 2075
184
185

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

197 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
198 1 5 10 15
199
200 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
201 20 25 30
202
203 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
204 35 40 45
205
206 Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
207 50 55 60
208
209 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
210 65 70 75 80
211
212 Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr

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	85	90	95
213			
214			
215	Ala Lys Asp Gly	Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser	
216	100	105	110
217			
218	Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp		
219	115	120	125
220			
221	Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro		
222	130	135	140
223			
224	Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys		
225	145	150	155
226			
227	Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly		
228	165	170	175
229			
230	Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro		
231	180	185	190
232			
233	Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala		
234	195	200	205
235			
236	Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp		
237	210	215	220
238			
239	Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg		
240	225	230	235
241			
242	Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys		
243	245	250	255
244			
245	Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly		
246	260	265	270
247			
248	Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr		
249	275	280	285
250			
251	Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu		
252	290	295	300
253			
254	Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile		
255	305	310	315
256			
257	Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe		
258	325	330	335
259			
260	Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala		
261	340	345	

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/752,427

DATE: 09/11/91
TIME: 09:53:06

LINE ERROR

ORIGINAL TEXT

28 Wrong application Serial Number

(A) APPLICATION NUMBER: US



PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/752,427

DATE: 09/11/91
TIME: 09:53:06

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/752,427

DATE: 09/11/91
TIME: 09:53:06

LINE ORIGINAL TEXT

CORRECTED TEXT